

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: WAHL, DR., GEOFFREY M.  
O'GORMAN DR., STEPHEN V.

(ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN  
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL  
THEREFOR

(iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
(B) STREET: 444 South Flower Street, Suite 2000  
(C) CITY: Los Angeles  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 90071

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/666,252  
(B) FILING DATE: 08-MAR-1991  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: REITER MR., STEPHEN E.  
(B) REGISTRATION NUMBER: 31192  
(C) REFERENCE/DOCKET NUMBER: P31 8929

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 535-9001  
(B) TELEFAX: (619) 535-8949

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

44 1814  
Entered

#12 4P  
OK

03-23-92

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54  
55 (vii) IMMEDIATE SOURCE:  
56 (B) CLONE: NATIVE FLP  
57  
58 (ix) FEATURE:  
59 (A) NAME/KEY: CDS  
60 (B) LOCATION: 1..1269  
61  
62  
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
64  
65 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 48  
66 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val  
67 1 5 10 15  
68  
69 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 96  
70 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala  
71 20 25 30  
72  
73 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144  
74 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn  
75 35 40 45  
76  
77 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 192  
78 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile  
79 50 55 60  
80  
81 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240  
82 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys  
83 65 70 75 80  
84  
85 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 288  
86 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu  
87 85 90 95  
88  
89 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 336  
90 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His  
91 100 105 110  
92  
93 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA 384  
94 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu  
95 115 120 125  
96  
97 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT 432  
98 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu  
99 130 135 140  
100  
101 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480  
102 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys  
103 145 150 155 160  
104  
105 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528  
106 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr

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	165	170	175	
107				
108				
109	TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC			576
110	Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe			
111	180	185	190	
112				
113	AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT			624
114	Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn			
115	195	200	205	
116				
117	AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA			672
118	Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr			
119	210	215	220	
120				
121	AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT			720
122	Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp			
123	225	230	235	240
124				
125	CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA			768
126	Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu			
127	245	250	255	
128				
129	AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC			816
130	Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr			
131	260	265	270	
132				
133	CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG			864
134	Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys			
135	275	280	285	
136				
137	AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT			912
138	Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser			
139	290	295	300	
140				
141	CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA			960
142	His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu			
143	305	310	315	320
144				
145	ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT			1008
146	Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser			
147	325	330	335	
148				
149	GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT			1056
150	Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp			
151	340	345	350	
152				
153	CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA			1104
154	His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser			
155	355	360	365	
156				
157	AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG			1152
158	Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp			
159	370	375	380	

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160  
161 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC 1200  
162 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr  
163 385 390 395 400  
164  
165 CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA 1248  
166 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser  
167 405 410 415  
168  
169 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT 1299  
170 Ser Tyr Ile Asn Arg Arg Ile  
171 420  
172  
173 ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 1359  
174  
175 ACAGTGAGCT GTATGTGCGC A 1380  
176  
177  
178 (2) INFORMATION FOR SEQ ID NO:2:  
179  
180 (i) SEQUENCE CHARACTERISTICS:  
181 (A) LENGTH: 423 amino acids  
182 (B) TYPE: amino acid  
183 (D) TOPOLOGY: linear  
184  
185 (ii) MOLECULE TYPE: protein  
186  
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
188  
189 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val  
190 1 5 10 15  
191  
192 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala  
193 20 25 30  
194  
195 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn  
196 35 40 45  
197  
198 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile  
199 50 55 60  
200  
201 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys  
202 65 70 75 80  
203  
204 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu  
205 85 90 95  
206  
207 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His  
208 100 105 110  
209  
210 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu  
211 115 120 125  
212

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213 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
214      130                      135                      140
215
216 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
217      145                      150                      155                      160
218
219 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
220                      165                      170                      175
221
222 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
223                      180                      185                      190
224
225 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
226      195                      200                      205
227
228 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
229      210                      215                      220
230
231 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
232      225                      230                      235                      240
233
234 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
235      245                      250                      255
236
237 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
238      260                      265                      270
239
240 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
241      275                      280                      285
242
243 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
244      290                      295                      300
245
246 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
247      305                      310                      315                      320
248
249 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
250      325                      330                      335
251
252 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
253      340                      345                      350
254
255 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
256      355                      360                      365
257
258 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
259      370                      375                      380
260
261 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
262      385                      390                      395                      400
263
264 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
265      405                      410                      415

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266

267 Ser Tyr Ile Asn Arg Arg Ile

268 420

269

270 (2) INFORMATION FOR SEQ ID NO:3:

271

272 (i) SEQUENCE CHARACTERISTICS:

273 (A) LENGTH: 34 base pairs

274 (B) TYPE: nucleic acid

275 (C) STRANDEDNESS: unknown

276 (D) TOPOLOGY: unknown

277

278 (ii) MOLECULE TYPE: cDNA

279

280 (vi) ORIGINAL SOURCE:

281 (C) INDIVIDUAL ISOLATE: FLP recombination target site

282

283

284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

285

286 GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

287

288 (2) INFORMATION FOR SEQ ID NO:4:

289

290 (i) SEQUENCE CHARACTERISTICS:

291 (A) LENGTH: 68 base pairs

292 (B) TYPE: nucleic acid

293 (C) STRANDEDNESS: unknown

294 (D) TOPOLOGY: unknown

295

296 (ii) MOLECULE TYPE: cDNA

297

298 (vi) ORIGINAL SOURCE:

299 (C) INDIVIDUAL ISOLATE: Synthetic oligonucleotide

300

301

302 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

303

304 GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG

60

305

306 GAACTTCA

68

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SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/666,252A

DATE: 03/17/92  
TIME: 10:30:05

LINE ERROR

ORIGINAL TEXT

30 Wrong application Serial Number

(A) APPLICATION NUMBER: US 07/666,252



PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/666,252A

DATE: 03/17/92  
TIME: 10:30:05

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE



PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/666,252A

DATE: 03/17/92  
TIME: 10:30:05

LINE ORIGINAL TEXT

CORRECTED TEXT